

Amendments to the Claims

1. (Currently Amended) A computer-implemented method for making allele calls, comprising:

receiving data representing nucleic acid information;

using a computer, applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and

depending on agreement between the results of ~~each algorithm~~ at least two of the algorithms, identifying an allele call within the data and assigning a confidence level for each call.

2. (original) The computer-implemented method of claim 1, wherein the allele calling algorithms applied in the step of applying at least two different allele calling algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

3. (currently amended) A computer-implemented for making allele calls, comprising:

receiving a signal representing nucleic acid information;

~~determining whether the signal is below a predefined complexity~~ using a computer, analyzing the signal to determine if the signal meets a threshold test of an allele caller making a correct call; and

making an allele call for the signal ~~based on the determination~~ if the threshold test is met.

4. (currently amended) A computer-implemented method for making allele calls, comprising:

receiving signal representing nucleic acid information;

using a computer, applying a set of filters to the signal to eliminate peaks that do not represent alleles, wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker; and

determining that remaining peaks in the data are alleles after applying the set of filters to the signal.

5. (original) The method of claim 4, wherein the applying step includes the substeps of:

creating a list of peaks in the signal;

determining characteristics associated with each peak; and

removing peaks from the list based on the determined characteristics.

6. (original) The method of any of claims 1, 3, or 4, wherein the nucleic acid information is nucleic acid length.

7. (Withdrawn) A computer-implemented method for interpreting nucleotide or amino acid information, comprising:

receiving data representing nucleotide or amino acid information;

applying at least two different algorithms to the data to provide a result for each algorithm; and

depending on agreement between the results of each algorithm, identifying at least one correct result within the data and assigning a confidence level to the at least one correct result.

8. (Withdrawn) The computer-implemented method of claim 7, wherein the algorithms applied in the step of applying at least two different algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

9. (currently amended) A computer-implemented method for making allele calls associated with data representing nucleic acid information, comprising:

using a computer, applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data;

if results from all of the applied allele calling algorithms are consistent, assigning a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms;

if results from all of the applied allele calling algorithms are not consistent, assigning different levels of confidence for any allele calls identified in the data during application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results; and

outputting a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

10. (original) The computer-implemented method of claim 9, wherein the allele calling algorithms applied in the applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data, are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

11. (currently amended) A system for making allele calls, comprising:
a processor configured to execute program instructions; and
a memory containing program instructions for execution by the processor to
receive data representing nucleic acid information,
apply at least two different allele calling algorithms to the data to provide a result for each algorithm, and
depending on agreement between the results of ~~each algorithm~~ at least two of the algorithms, identify an allele call within the data and assigning a confidence level for each call.

12. (original) The computer-implemented method of claim 11, wherein the allele calling algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

13. (original) The system of claim 11, wherein the nucleic acid information comprises nucleic acid length.

14. (currently amended) A system for making allele calls, comprising:

a processor configured to execute program instructions; and
a memory containing program instructions for execution by the processor to
receive a signal representing nucleic acid information,
~~determine whether the signal is below a predefined complexity~~ analyze the signal
to determine if the signal meets a threshold test of an allele caller making a correct call, and
make an allele call for the signal ~~based on the determination~~ if the threshold test is
met.

15. (original) The system of claim 14, wherein the nucleic acid information comprises nucleic acid length.

16. (original) A system for making allele calls, comprising:
a processor configured to execute program instructions; and
a memory containing program instructions for execution by the processor to
receive signal representing nucleic acid information,
apply a set of filters to the signal to eliminate peaks that do not represent alleles,
wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker, and
determine that remaining peaks in the data are alleles after applying the set of filters to the signal.

17. (original) The system of claim 16, wherein when the processor executing program instructions applies the set of filters to the signal to eliminate peaks that do not represent alleles, the processor creates a list of peaks in the signal, determines characteristics associated with each peak, and removes peaks from the list based on the determined characteristics.

18. (original) The system of claim 16, wherein the nucleic acid information comprises nucleic acid length.

19. (Withdrawn) A system for interpreting nucleotide or amino acid information, comprising:

a processor to execute program instructions; and

a memory that stores program instructions for execution by the processor to

receive data representing nucleotide or amino acid information,

apply at least two different algorithms to the data to provide a result for each algorithm, and

depending on agreement between the results of each algorithm, identify at least one correct result within the data and assigning a confidence level to the at least one correct result.

20. (Withdrawn) The system of claim 19, wherein the algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

21. (original) A system for making allele calls associated with data representing nucleic acid information, comprising:

a processor to execute program instructions; and

a memory that stores program instructions for execution by the processor to

apply each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data,

if results from all of the applied allele calling algorithms are consistent, assign a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms,

if results from all of the applied allele calling algorithms are not consistent, assign different levels of confidence for any allele calls identified in the data during application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results, and

output a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

22. (original) The system of claim 21, wherein the allele calling algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

23. (currently amended) A computer readable medium containing instructions for controlling a computer system to perform a method for making correct allele calls, the method comprising:

receiving data representing nucleic acid information;

applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and

depending on agreement between the results of ~~each algorithm~~ at least two of the algorithms, identifying an allele call within the data and assigning a confidence level for each call.

24. (original) The computer readable medium of claim 23, wherein the allele calling algorithms applied in the applying of at least two different allele calling algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

25. (currently amended) A computer readable medium containing instructions for controlling a computer system to perform a method for making allele calls, the method comprising:

receiving a signal representing nucleic acid information,

~~determining whether the signal is below a predefined complexity~~ analyzing the signal to determine if the signal meets a threshold test of an allele caller making a correct call, and making an allele call for the signal ~~based on the determination~~ if the threshold test is met.

26. (original) A computer readable medium containing instructions for controlling a computer system to perform a method for making allele calls, the method comprising:
- receiving signal representing nucleic acid information;
 - applying a set of filters to the signal to eliminate peaks that do not represent alleles, wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker; and
 - determining that remaining peaks in the data are alleles after applying the set of filters to the signal.
27. (original) The computer readable medium of claim 26, wherein the applying of the set of filters includes:
- creating a list of peaks in the signal;
 - determining characteristics associated with each peak; and
 - removing peaks from the list based on the determined characteristics.
28. (original) The method of any of claims 23, 25, or 26, wherein the nucleic acid information is nucleic acid length.
29. (Withdrawn) A computer readable medium containing instructions for controlling a computer system to perform a method for interpreting nucleotide or amino acid information, the method comprising:

receiving data representing nucleotide or amino acid information;
applying at least two different algorithms to the data to provide a result for each algorithm; and

depending on agreement between the results of each algorithm, identifying at least one correct result within the data and assigning a confidence level to the at least one correct result.

30. (Withdrawn) The computer readable medium of claim 29, wherein the algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

31. (Withdrawn) A computer readable medium containing instructions for controlling a computer system to perform a method for making allele calls associated with data representing nucleic acid information, the method comprising:

applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data;

if results from all of the applied allele calling algorithms are consistent, assigning a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms;

if results from all of the applied allele calling algorithms are not consistent, assigning different levels of confidence for any allele calls identified in the data during application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results; and

outputting a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

32. (Withdrawn) The computer readable medium of claim 31, wherein the allele calling algorithms applied in the applying of each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data, are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

33. (currently amended) A system for making allele calls, comprising:
means for receiving data representing nucleic acid information;
means for applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and
means for depending on agreement between the results of ~~each algorithm~~ at least two of the algorithms, identifying an allele call within the data and assigning a confidence level for each call.

34. (Withdrawn) A computer-implemented method for obtaining an allele call report, comprising:
receiving data representing nucleic acid information;
applying at least two different algorithms to the data to provide an allele call report;

generating a first algorithm quality value based on one of the at least two different algorithms;

generating a second algorithm quality value based on another of the at least two different algorithms;

generating an allele call report quality value based on at least the first and second algorithm quality values; and

predicting the accuracy of allele call report in view of the generated allele call report quality value.

35. (Withdrawn) The computer-implemented method of claim 34, wherein the applying of the at least two different algorithms comprises applying at least two of the following algorithms a) through c):

a) a preprocessing algorithm, comprising at least one of an offscale detection algorithm, a multicomponenting algorithm, and a baselining algorithm;

b) a data conversion algorithm, comprising at least one of a peak detecting algorithm, a size standard matching algorithm, and a size calling algorithm; and

c) an allele call reporting algorithm, comprising at least one of an allele calling algorithm, an auto binning algorithm, and a bin assigning algorithm.

36. (Withdrawn) The computer-implemented method of claim 35, wherein the generating of the first and second quality values comprises generating a quality value for the data conversion algorithm and generating a quality value for the allele call reporting algorithm.

37. (Withdrawn) The computer-implemented method of claim 35, wherein the applying of the at least two different algorithms comprises applying:
- a data conversion algorithm, comprising at least one of a peak detecting algorithm, a size standard matching algorithm, and a size calling algorithm; and
 - an allele call reporting algorithm, comprising at least one of an allele calling algorithm, an auto binning algorithm, and a bin assigning algorithm.
38. (Withdrawn) The computer-implemented method of claim 37, wherein the generating of the first and second algorithm quality values comprises generating a quality value for the data conversion algorithm and generating a quality value for the allele call reporting algorithm.
39. (Withdrawn) The computer-implemented method of claim 35, wherein the applying of the at least two different algorithms comprises applying:
- a data conversion algorithm, comprising a peak detecting algorithm, a size standard matching algorithm, and a size calling algorithm; and
 - an allele call reporting algorithm, comprising an allele calling algorithm.
40. (Withdrawn) The computer-implemented method of claim 39, wherein the generating of the first and second algorithm quality values comprises generating a quality value for the data conversion algorithm by a process comprising generating a quality value for the size standard matching algorithm, and generating a quality value for the allele call reporting algorithm by a process comprising generating a quality value for the allele calling algorithm.

41. (Withdrawn) The computer-implemented method of claim 35, wherein the applying of the at least two different algorithms comprises applying:

a data conversion algorithm, comprising a peak detecting algorithm, a size standard matching algorithm, and a size calling algorithm; and

an allele call reporting algorithm, comprising an allele calling algorithm and a bin assigning algorithm.

42. (Withdrawn) The computer-implemented method of claim 41, wherein the generating of the first and second algorithm quality values comprises generating a quality value for the data conversion algorithm by a process comprising generating a quality value for the size standard matching algorithm, and generating a quality value for the allele call reporting algorithm by a process comprising generating a quality value for the allele calling algorithm.

43. (Withdrawn) The computer-implemented method of claim 42, wherein the process for generating a quality value for the allele call reporting algorithm further comprises generating a quality value for the bin assigning algorithm, and generating the quality value for the allele call reporting algorithm based on the quality value for the allele calling algorithm and the quality value for the bin assigning algorithm.

44. (Withdrawn) The computer-implemented method of claim 35, wherein the applying of the at least two different algorithms comprises applying:

a data conversion algorithm, comprising a peak detecting algorithm, a size standard matching algorithm, and a size calling algorithm; and

an allele call reporting algorithm, comprising an allele calling algorithm, an auto binning algorithm, and a bin assigning algorithm.

45. (Withdrawn) The computer-implemented method of claim 44, wherein the generating of the first and second algorithm quality values comprises generating a quality value for the data conversion algorithm by a process comprising generating a quality value for the size standard matching algorithm, and generating a quality value for the allele call reporting algorithm by a process comprising generating a quality value for the allele calling algorithm.

46. (Withdrawn) The computer-implemented method of claim 45, wherein the process for generating a quality value for the allele call reporting algorithm further comprises generating a quality value for the bin assigning algorithm, and generating the quality value for the allele call reporting algorithm based on the quality value for the allele calling algorithm and the quality value for the bin assigning algorithm.

47. (Withdrawn) The computer-implemented method of claim 46, wherein the process for generating a quality value for the allele call reporting algorithm further comprises generating a quality value for the auto binning algorithm, and generating the quality value for the allele call reporting algorithm based on the quality value for the allele calling algorithm, the quality value for the bin assigning algorithm, and the quality value of the auto binning algorithm.

48. (Withdrawn) The computer-implemented method of claim 34, wherein the applying of the at least two different algorithms comprises applying:

a preprocessing algorithm, comprising at least one of an offscale detection algorithm, a multicomponenting algorithm, and a baselining algorithm;

a data conversion algorithm, comprising at least one of a peak detecting algorithm, a size standard matching algorithm, and a size calling algorithm; and

an allele call reporting algorithm, comprising at least one of an allele calling algorithm, an auto binning algorithm, and a bin assigning algorithm.

49. (Withdrawn) The computer-implemented method of claim 48, wherein the generating of the first and second algorithm quality values comprises generating a quality value for the data conversion algorithm and generating a quality value for the allele call reporting algorithm.

50. (Withdrawn) The computer-implemented method of claim 49, further comprising generating a third algorithm quality value, which comprises generating a quality value for the preprocessing algorithm, and generating an allele call report quality value based on at least the first, second, and third algorithm quality values.

51. (Withdrawn) The computer-implemented method of claim 48, wherein the applying of the at least two different algorithms comprises applying:

a preprocessing algorithm, comprising at least one of an offscale detection algorithm, a multicomponenting algorithm, and a baselining algorithm;

a data conversion algorithm, comprising a peak detecting algorithm, a size standard matching algorithm, and a size calling algorithm; and

an allele call reporting algorithm, comprising an allele calling algorithm and a bin assigning algorithm.

52. (Withdrawn) The computer-implemented method of claim 51, wherein the generating of the first and second algorithm quality values comprises generating a quality value for the data conversion algorithm by a process comprising generating a quality value for the size standard matching algorithm, and generating a quality value for the allele call reporting algorithm by a process comprising generating a quality value for the allele calling algorithm.

53. (Withdrawn) The computer-implemented method of claim 52, wherein the process for generating a quality value for the allele call reporting algorithm further comprises generating a quality value for the bin assigning algorithm, and generating the quality value for the allele call reporting algorithm based on the quality value for the allele calling algorithm and the quality value for the bin assigning algorithm.

54. (Withdrawn) The computer-implemented method of claim 35, wherein the applying of the at least two different algorithms comprises applying:

a data conversion algorithm, comprising a peak detecting algorithm, a size standard matching algorithm, and a size calling algorithm; and

an allele call reporting algorithm, comprising applying at least two different allele calling algorithms to provide a result for each algorithm.

55. (Withdrawn) The computer-implemented method of claim 54, wherein the generating of the first and second algorithm quality values comprises generating a quality value for the data conversion algorithm by a process comprising generating a quality value for the size standard matching algorithm, and generating a quality value for the allele call reporting algorithm by a process comprising generating a quality value for the allele calling algorithm based on the results of each of the at least two different allele calling algorithms.

56. (Withdrawn) The computer-implemented method of claim 34, wherein the applying of the at least two different algorithms comprises applying:

a data conversion algorithm, comprising a peak detecting algorithm, a ladder shift algorithm, and a size calling algorithm; and

an allele call reporting algorithm, comprising an allele calling algorithm and a bin assigning algorithm.

57. (Withdrawn) The computer-implemented method of claim 56, wherein the generating of the first and second algorithm quality values comprises generating a quality value for the data conversion algorithm by a process comprising generating a quality value for the ladder shift algorithm, and generating a quality value for the allele call reporting algorithm by a process comprising generating a quality value for the bin assigning algorithm.

58. (Withdrawn) The computer-implemented method of claim 34, wherein the applying of the at least two different algorithms comprises applying at least two of the following algorithms:

- an offscale detection algorithm;
- a multicomponenting algorithm;
- a peak detecting algorithm;
- a baselining algorithm;
- a size standard matching algorithm;
- a size calling algorithm;
- an allele calling algorithm;
- an auto binning algorithm; and
- a bin assigning algorithm.

59. (Withdrawn) The computer-implemented method of claim 58, wherein the applying of the at least two different algorithms comprises applying a baselining algorithm, a size standard matching algorithm, a size calling algorithm, an allele calling algorithm, and a bin assigning algorithm.

60. (Withdrawn) The computer-implemented method of claim 59, wherein the generating of the first and second algorithm quality values comprises generating a quality value for a size standard matching algorithm and an allele calling algorithm.

61. (Withdrawn) The computer-implemented method of claim 60, further comprising generating a third algorithm quality value, which comprises generating a quality value for the bin assigning algorithm, and generating an allele call report quality value based on at least the first, second, and third algorithm quality values.

62. (Withdrawn) A system for making allele calls, comprising:
a processor configured to execute program instructions; and
a memory containing program instructions for execution by the processor to
receive data representing nucleic acid information,
apply at least two different algorithms to the data to provide an allele call
report;
generate a first algorithm quality value based on one of the at least two
different algorithms;
generate a second algorithm quality value based on another of the at least
two different algorithms;
generate an allele call report quality value based on at least the first and second
algorithm quality values; and
predict the accuracy of allele call report in view of the generated allele call
report quality value.

63. (Withdrawn) A computer readable medium containing instructions for
controlling a computer system to perform a method of making allele calls, the method
comprising:

receiving data representing nucleic acid information;

applying at least two different algorithms to the data to provide an allele call report;

generating a first algorithm quality value based on one of the at least two different algorithms;

generating a second algorithm quality value based on another of the at least two different algorithms;

generating an allele call report quality value based on at least the first and second algorithm quality values; and

predicting the accuracy of allele call report in view of the generated allele call report quality value.